

#10

1110-0266P.ST25
SEQUENCE LISTING

<110> NAGATA, Shigekazu et al.

<120> Novel Fas Ligand Derivative

<130> 1110-0266P

<140> 09/508,849

<141> 2000-03-17

<150> JP P1997-252541

<151> 1997-09-17

<160> 16

<170> PatentIn Ver. 2.1

<210> 1

<211> 258

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:amino acids at
111-133 from N terminal are deleted from natural
human Fas ligand

<400> 1

Met	Gln	Gln	Pro	Phe	Asn	Tyr	Pro	Tyr	Pro	Gln	Ile	Tyr	Trp	Val	Asp
1				5					10					15	

Ser	Ser	Ala	Ser	Ser	Pro	Trp	Ala	Pro	Pro	Gly	Thr	Val	Leu	Pro	Cys
			20					25					30		

Pro	Thr	Ser	Val	Pro	Arg	Arg	Pro	Gly	Gln	Arg	Arg	Pro	Pro	Pro	Pro
		35					40					45			

Pro	Pro	Pro	Pro	Pro	Leu	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Leu	Pro
		50				55					60				

Pro	Leu	Pro	Leu	Pro	Pro	Leu	Lys	Lys	Arg	Gly	Asn	His	Ser	Thr	Gly
65					70					75					80

Leu	Cys	Leu	Leu	Val	Met	Phe	Phe	Met	Val	Leu	Val	Ala	Leu	Val	Gly
				85					90					95	

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Leu	Gly	Leu	Gly	Met	Phe	Gln	Leu	Phe	His	Leu	Gln	Lys	Glu	Pro	Ser		
			100					105					110				
Pro	Pro	Pro	Glu	Lys	Lys	Glu	Leu	Arg	Lys	Val	Ala	His	Leu	Thr	Gly		
		115					120					125					
Lys	Ser	Asn	Ser	Arg	Ser	Met	Pro	Leu	Glu	Trp	Glu	Asp	Thr	Tyr	Gly		
	130					135					140						
Ile	Val	Leu	Leu	Ser	Gly	Val	Lys	Tyr	Lys	Lys	Gly	Gly	Leu	Val	Ile		
145					150					155					160		
Asn	Glu	Thr	Gly	Leu	Tyr	Phe	Val	Tyr	Ser	Lys	Val	Tyr	Phe	Arg	Gly		
				165					170					175			
Gln	Ser	Cys	Asn	Asn	Leu	Pro	Leu	Ser	His	Lys	Val	Tyr	Met	Arg	Asn		
			180					185					190				
Ser	Lys	Tyr	Pro	Gln	Asp	Leu	Val	Met	Met	Glu	Gly	Lys	Met	Met	Ser		
	195						200					205					
Tyr	Cys	Thr	Thr	Gly	Gln	Met	Trp	Ala	Arg	Ser	Ser	Tyr	Leu	Gly	Ala		
	210					215					220						
Val	Phe	Asn	Leu	Thr	Ser	Ala	Asp	His	Leu	Tyr	Val	Asn	Val	Ser	Glu		
225					230					235					240		
Leu	Ser	Leu	Val	Asn	Phe	Glu	Glu	Ser	Gln	Thr	Phe	Phe	Gly	Leu	Tyr		
				245					250					255			
Lys	Leu																

<210> 2

<211> 277

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:amino acids at
128-131 from N terminal are deleted from natural
human Fas ligang

<400> 2

Met	Gln	Gln	Pro	Phe	Asn	Tyr	Pro	Tyr	Pro	Gln	Ile	Tyr	Trp	Val	Asp		
1				5					10					15			

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Ser	Ser	Ala	Ser	Ser	Pro	Trp	Ala	Pro	Pro	Gly	Thr	Val	Leu	Pro	Cys
			20					25					30		
Pro	Thr	Ser	Val	Pro	Arg	Arg	Pro	Gly	Gln	Arg	Arg	Pro	Pro	Pro	Pro
		35					40					45			
Pro	Pro	Pro	Pro	Pro	Leu	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Leu	Pro
	50					55					60				
Pro	Leu	Pro	Leu	Pro	Pro	Leu	Lys	Lys	Arg	Gly	Asn	His	Ser	Thr	Gly
65					70					75					80
Leu	Cys	Leu	Leu	Val	Met	Phe	Phe	Met	Val	Leu	Val	Ala	Leu	Val	Gly
				85					90					95	
Leu	Gly	Leu	Gly	Met	Phe	Gln	Leu	Phe	His	Leu	Gln	Lys	Glu	Leu	Ala
			100					105					110		
Glu	Leu	Arg	Glu	Ser	Thr	Ser	Gln	Met	His	Thr	Ala	Ser	Ser	Leu	Gly
		115					120					125			
His	Pro	Ser	Pro	Pro	Pro	Glu	Lys	Lys	Glu	Leu	Arg	Lys	Val	Ala	His
	130					135					140				
Leu	Thr	Gly	Lys	Ser	Asn	Ser	Arg	Ser	Met	Pro	Leu	Glu	Trp	Glu	Asp
145					150					155					160
Thr	Tyr	Gly	Ile	Val	Leu	Leu	Ser	Gly	Val	Lys	Tyr	Lys	Lys	Gly	Gly
				165					170					175	
Leu	Val	Ile	Asn	Glu	Thr	Gly	Leu	Tyr	Phe	Val	Tyr	Ser	Lys	Val	Tyr
			180					185					190		
Phe	Arg	Gly	Gln	Ser	Cys	Asn	Asn	Leu	Pro	Leu	Ser	His	Lys	Val	Tyr
		195					200					205			
Met	Arg	Asn	Ser	Lys	Tyr	Pro	Gln	Asp	Leu	Val	Met	Met	Glu	Gly	Lys
	210					215					220				
Met	Met	Ser	Tyr	Cys	Thr	Thr	Gly	Gln	Met	Trp	Ala	Arg	Ser	Ser	Tyr
225					230					235					240
Leu	Gly	Ala	Val	Phe	Asn	Leu	Thr	Ser	Ala	Asp	His	Leu	Tyr	Val	Asn
				245					250					255	
Val	Ser	Glu	Leu	Ser	Leu	Val	Asn	Phe	Glu	Glu	Ser	Gln	Thr	Phe	Phe
			260					265					270		

Gly Leu Tyr Lys Leu
275

<210> 3

<211> 281

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:point mutation
of a substitution of Lys 129 for Ala from N
terminal is present in natural human Fas ligand
<D6>

<400> 3

Met Gln Gln Pro Phe Asn Tyr Pro Tyr Pro Gln Ile Tyr Trp Val Asp
1 5 10 15

Ser Ser Ala Ser Ser Pro Trp Ala Pro Pro Gly Thr Val Leu Pro Cys
20 25 30

Pro Thr Ser Val Pro Arg Arg Pro Gly Gln Arg Arg Pro Pro Pro Pro
35 40 45

Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro Pro Leu Pro
50 55 60

Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg Gly Asn His Ser Thr Gly
65 70 75 80

Leu Cys Leu Leu Val Met Phe Phe Met Val Leu Val Ala Leu Val Gly
85 90 95

Leu Gly Leu Gly Met Phe Gln Leu Phe His Leu Gln Lys Glu Leu Ala
100 105 110

Glu Leu Arg Glu Ser Thr Ser Gln Met His Thr Ala Ser Ser Leu Glu
115 120 125

Ala Gln Ile Gly His Pro Ser Pro Pro Pro Glu Lys Lys Glu Leu Arg
130 135 140

Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg Ser Met Pro Leu
145 150 155 160

Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly Val Lys Tyr
165 170 175

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Lys	Lys	Gly	Gly	Leu	Val	Ile	Asn	Glu	Thr	Gly	Leu	Tyr	Phe	Val	Tyr
		180						185					190		
Ser	Lys	Val	Tyr	Phe	Arg	Gly	Gln	Ser	Cys	Asn	Asn	Leu	Pro	Leu	Ser
		195					200					205			
His	Lys	Val	Tyr	Met	Arg	Asn	Ser	Lys	Tyr	Pro	Gln	Asp	Leu	Val	Met
	210					215					220				
Met	Glu	Gly	Lys	Met	Met	Ser	Tyr	Cys	Thr	Thr	Gly	Gln	Met	Trp	Ala
225					230					235					240
Arg	Ser	Ser	Tyr	Leu	Gly	Ala	Val	Phe	Asn	Leu	Thr	Ser	Ala	Asp	His
				245					250					255	
Leu	Tyr	Val	Asn	Val	Ser	Glu	Leu	Ser	Leu	Val	Asn	Phe	Glu	Glu	Ser
			260					265					270		
Gln	Thr	Phe	Phe	Gly	Leu	Tyr	Lys	Leu							
		275					280								

<210> 4

<211> 774

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DNA coding for
amino acids SEQ ID No.1

<400> 4

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atgcagcagc ctttcaatta cccatatccc cagatctact gggtaggacag cagtgccagc 60
tctccctggg cccctccagg cacagttctt ccctgtccaa cctctgtgcc cagaaggcct 120
gggtcaaagga ggccaccacc accaccgcca ccgccaccac taccacctcc gccgccgccg 180
ccaccactgc ctccactacc gctgccaccc ctgaagaaga gagggaacca cagcacaggc 240
ctgtgtctcc ttgtgatgtt tttcatgggt ctggttgctt tggtaggatt gggcctgggg 300
atgtttcagc ttttccacct acagaaggag ccagtgccac cccctgaaaa aaaggagctg 360
aggaaagtgg cccatttaac aggcaagtcc aactcaaggt ccatgcctct ggaatgggaa 420
gacacctatg gaattgtcct gctttctgga gtgaagtata agaagggtgg ccttgtgatc 480

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aatgaaactg ggctgtactt tgtatatcc aaagtatact tccgggggtca atcttgcaac 540
aacctgcccc tgagccacaa ggtctacatg aggaactcta agtatcccca ggatctgggtg 600
atgatggagg ggaagatgat gagctactgc actactgggc agatgtgggc ccgcagcagc 660
tacctggggg cagtgttcaa tcttaccagt gctgatcatt tatatgtcaa cgtatctgag 720
ctctctctgg tcaattttga ggaatctcag acgtttttcg gcttatataa gctc 774

<210> 5

<211> 831

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DNA coding for
amino acids SEQ ID No.2

<400> 5

atgcagcagc ccttcaatta cccatatccc cagatctact ggggtggacag cagtgccagc 60
tctccctggg cccctccagg cacagttctt ccctgtccaa cctctgtgcc cagaaggcct 120
gggtcaaagga ggccaccacc accaccgcca ccgccaccac taccacctcc gccgccgccg 180
ccaccactgc ctccactacc gctgccaccc ctgaagaaga gagggaaacca cagcacaggc 240
ctgtgtctcc ttgtgatgtt tttcatgggt ctggttgcct tggtaggatt gggcctgggg 300
atgttttcagc tcttccacct acagaaggag ctggcagaac tccgagagtc taccagccag 360
atgcacacag catcatcttt gggccacccc agtccacccc ctgaaaaaaaa ggagctgagg 420
aaagtggccc atttaacagg caagtccaac tcaaggtcca tgcctctgga atgggaagac 480
acctatggaa ttgtcctgct ttctggagtg aagtataaga agggtagcct tgtgatcaat 540
gaaactgggc tgtactttgt atattccaaa gtatacttcc ggggtcaatc ttgcaacaac 600
ctgcccctga gccacaaggt ctacatgagg aactctaagt atccccagga tctgggtgatg 660
atggagggga agatgatgag ctactgcact actgggcaga tgtgggcccg cagcagctac 720
ctgggggagc tgttcaatct taccagtgtc gatcatttat atgtcaacgt atctgagctc 780

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tctctggtca attttgagga atctcagacg tttttcggct tatataagct c

831

<210> 6

<211> 843

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DNA coding for
amino acids SEQ ID No.3

<400> 6

atgcagcagc ctttcaatta cccatatccc cagatctact ggggtggacag cagtgccagc 60
tctccctggg cccctccagg cacagttctt ccctgtccaa cctctgtgcc cagaaggcct 120
gggtcaaagga ggccaccacc accaccgcca ccgccaccac taccacctcc gccgccgccg 180
ccaccactgc ctccactacc gctgccaccc ctgaagaaga gagggaaacca cagcacaggc 240
ctgtgtctcc ttgtgatgtt tttcatgggt ctggttgcct tggtaggatt gggcctgggg 300
atgtttcagc tcttccacct acagaaggag ctggcagaac tccgagagtc taccagccag 360
atgcacacag catcatcttt ggaggcacia ataggccacc ccagtccacc ccctgaaaaa 420
aaggagctga ggaaagtggc ccatttaaca ggcaagtcca actcaaggtc catgcctctg 480
gaatgggaag acacctatgg aattgtcctg ctttctggag tgaagtataa gaaggggtggc 540
cttgtgatca atgaaactgg gctgtacttt gtatattcca aagtatactt ccgggggtcaa 600
tcttgcaaca acctgcccct gagccacaag gtctacatga ggaactctaa gtatccccag 660
gatctggtga tgatggaggg gaagatgatg agctactgca ctactgggca gatgtgggcc 720
cgcagcagct acctgggggc agtgttcaat cttaccagtg ctgatcattt atatgtcaac 780
gtatctgagc tctctctggg caattttgag gaatctcaga cgtttttcgg cttatataag 840
ctc 843

<210> 7

<211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:a sense primer
 BOS6

<400> 7
 cctcagacag tggttcaaag

20

<210> 8
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:an antisense
 deletion primer DA4

<400> 8
 ttttcagggg gtggactggg ctccttctgt aggtggaag

39

<210> 9
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:HFLP3

<400> 9
 gctctagaac attctcggtg cctgtaac

28

<210> 10
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DA5

<400> 10

tggactgggg tggcccaaag atgatgctgt

30

<210> 11

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DA6

<400> 11

ggggtggcct atttgtgcct ccaaagatga tgc

33

<210> 12

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:sequence of
human FasL from amino acids 130 to137

<400> 12

Gln Ile Gly His Pro Ser Pro Pro

1

5

<210> 13

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:the amino acid
sequence around the cleavage site of FasL

<400> 13

Glu Lys Gln Ile

1

<210> 14

<211> 8

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:the cleavage
site of THN-alpha

<400> 14
Leu Ala Gln Ala Val Arg Ser Ser
1 5

<210> 15
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:the cleavage
site of CD40

<400> 15
Asn Ser Phe Glu Met Gln Lys Gly
1 5

<210> 16
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:the cleavage
site of FasL

<400> 16
Ser Leu Glu Lys Gln Ile Gly His
1 5